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FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGMEH
RNHLCFCDLYDRATSPPLKCSLL

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FIGURE 439

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAACTAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTCAGAACAAAGCTTCCTGGAACCCATGACCCATGAAGTCTTGTGCGACATTTATACCGT
CTGAGGGTAGCAGCTCGAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTTGTGTGACCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTCACACTGGCTTGCCCTCCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA
AGGATGAATGTAACCTGGCGCCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
CACGGGACCTCGTCATCACTGCCCTTAACAACACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCCTGCG
GGGCTGTGGCCAGCGTCCAGCCACTGTGACACTAGCCAACTCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
ATTGAAGTGGATGAGGGAACACAGCAGTCAATGGCTGCCACCTGCCAGAGCCACCCCAAAGCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAGAAC
TCCGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCCGCATCACTACCCCGAGGGCC
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCCACCCCAAGGCTC
ACCTGGGCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
ACCACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTGGGCGAGCCCGGGCGAGCGGTC
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTCACTCCCTGGGGC
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
CTCATCTCCAGCCAGCGCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGGCTGAGGACGAAGGC
GTCTACAGTGCATGGCCGAGAACGAGGTGGGAGCGGCCATGCCGTAGTCCAGTCCAGCTCCAGGCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGCGCTCCCGAGACCCCAACGTCAGTGGGGCTGCTTCCCGGAAGTGT
CCAGGAGAGAAAGGGCGAGGGGCTCCCGCGAGGCTCCCATCTCAGCTCGCCCGCACCTCCAAGACAGAC
TCATATGAAGTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC
CGCAAGCAGTCAAAATCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACAGCAGCCGCTGACCTC
ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAACCTGTGCGGGAGAGGGCCAGACAGCC
ATGGTCACCTTCCGAACCTGGACGGCGGCCCAACCCGAGATCATGGCCAGCAAGAGAGCAGCATCCAGAGAGAC
GACCTTGGAGCCAGTCCCAGAGCAGCAGCCAGCCAGACACGGCCGCTCTCCCCCAGAAAGCTCCCGACAGG
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCGCCGTGGGAATGGTGGGTTCCTCAAT
CAGTCTTCCGTGTGGAGTACAAGAAGCTAAGAAAGTGGGAGACTGGATTCTGGCCACAGCGCCATCCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGTACAGCGGTGCGGTGTACGAGAGG
CCCGTGGCAGGTCTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACGATGACATGATAGT
GACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC
GACATTAAGATGCAGTCTTCAATGAAGGAGGGGAGAGCGAGTTGAGCAACGTGATGATCTGTGAGACCAAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTCTGACTGCCACCCCAACTCTGGCCCAACACAGCGCCGCTCTCTGAAACC
ATAGAGCGCGCGGTGGGCACCTGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTG
CTGGGCTCCATCGTTCTCATCATCGTCACTTCATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGGCTTCCACCTCCTGCCGTATACTATGGTGGCATTTGGGAGGACTC
CCAGGCCACAGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCGGGCATGAAGCCCAAGCAGCACTGCCAGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCTGCTGAGGCGAGCCATCTTGGCAATGGATATGACCCCAAGTCAACAGATC
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTTTTCTTATACACACTGCCGAGACTCCACTCACCAGCTG
CTGCAGCCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAAGGGTGGAGAGGCC
CCCGACAGTCTGTCTGGAAGCAGTGTGGGACCCCTCAATTCACCTCAGGCCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCCGTAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCGCACTGGTGGTGTGCTTTTGAACACCCACT
CTCACAATTTAGGCAGAAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAAAGAAAAA
AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGAAAAATAAGAAGCTGCCA
CCTAACAGGAGTCAACAGGAAAGCACCGCACAGGCTGGCGGGGACAGACTCCTAACCTGGGCGCTGTGAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGTGGCAAGAGGAAGGATCCAGGCACATGGTTCAACAGGCA
TGAGGGAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGCTACGGGAA
ACATTTTCTAAGATGCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAAAAACCTTCAGAAAT
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACTGTAACCTCTAAATAAATGTTAGTCTTCCTGTAAAA

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FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGAAVILY
NVQVFEPPEVTMELSOLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCMAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGEGKGQGAPEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGASPOSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRVRALNMLGESEP
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIIPASNNNTPIHGFIYYRPT
DSDNDS DYKKDMVEGD KYWHSISHLQ PETSYDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLFYLIIVGVVLGSIVLIIVTFIPFCLWRAW
SKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCP SAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTLPPDS
THQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDP PFHSGPPCCLGLVPVEEVDS PD
SCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

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FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCACTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTTCCTGCTGGATGGTTTTCTGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCTGGGAAACACTCTGAGATATATA
ACAAACTGAGCACAGTGGAAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

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FIGURE 442

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDYL
TPDFPSLSYPNYITLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMPLWWNGSEPLWVT
LTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAAYH
ERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWQIQRGLQDRNLNVIIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

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FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCAATGAGGATCATGCTGCTATTACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATTAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTCCCTGTTCTTGTAACATTCTTGTG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATAACCCTAGAGTTCCTGTAGTGTCTACATTAAAAAT
ATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCAGTCCACCAATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCCTGTGCGCACGCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

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FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCGSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVIINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCTGCGTGCTGCC
CCGTTCACTGTGACCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAACTGATGAACACATCCCCAAA

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FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGOALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYYRVDTDDEDRYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 449

TGCAGAGCCTTGTGGAGGCCATGGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGGCCCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGT CATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCCGCTTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAACCTGAGACTCGTTTCAGACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTGGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAAATTGGCCTTAATACAGTTTTTAAC
CACTGATAATTCAGATTTGTTCAATTAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTGATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCCGAGAAATGCCCCCTCATCATTTCCATGATCGACTTTATTA
CCTCAATGGCATAAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAAGCCACACACG
TGCACCTCCTTGCCATATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAAACTTAAACTGAACTATGAAGTGACACACTCCTTTTTCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

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FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDPKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGOEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETLOKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTAKQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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FIGURE 451

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCTCAAAATGG
CATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTCCC
CGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCAACCTGCCTCACAGG
TGTATTCCCTCAACACCGACTTTGCCTTCGGCCTATAACCGCAGGCTGGTTTTGGAGACCCCGA
GTCAGAACATCTTCTTCTCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCTTGGGG
CCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACACACCAG
AGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCAGCAAAGACC
TGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGCAAATTTCT
TGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTCTACAGATTTCTCCAACCCCTCCA
TTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAAGACCCAAGGGAAGGTTGTAGACATAA
TCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTTTAAAGCCAAAGT
GGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGG
TCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGC
TGAAGTGTCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCCTCCCTA
GCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACACTGATAAAGTGGAGCC
ACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCCATTTCTGCCTCCTACA
ATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAATGCTGATTTTTT
CTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATG
TCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGG
ATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCCTGATGATGATTACAAATAAAG
CCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCACTAAATCCTAGGTGGGAAATG
GCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCTCTTTCTGT
TCTGAGGGTGCATTTGACCCAGTGGAGCTGGATTGCTGGCAGGGATGCCACTTCCAAGGCT
CAATCACCAAACCATCAACAGGGACCCAGTCACAAGCCAACACCCATTAACCCAGTCAGTG
CCCTTTTCCACAAATTCTCCAGGTAAGTCTCATGGGATGTTGCTGGGTTACCATATTTT
CATTCTTGGGGCTCCCAGGAATGGAAATACGCCAACCCAGGTTAGGCACCTCTATTGCAGAA
TTACAATAACACATTCAATAAACTAAAATATGAATTCAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

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FIGURE 452

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLOKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

FIGURE 453

CTCCGGGTTCCCAAGGGGCTGCGCCGGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCGGAGGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGA GTCCGGCCGAGCCACTGAGCCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCCGCGATGGGCGCTGAGGAGCTGGCTCGCCGCCCTCAGGGCGCGCTGCCG
CTCTCGGCACCGCTGCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCAGCCGCGCCTCCGACCTGGGCGCTCAGC
CCCCGGATACGACCTGCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAAGCTGAACACATCTCCAACATC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAAGTACATCAAGATCCTCTGCGCGCTCAGCGGCAGTCA
CTGTTCACTTGTGGCACAGACCTTCAAGCCCATGTGCTACCTACATCAACATCGAGAATTCACCTTGGCAAG
GACGAGAAGGGATGTCTCTCTGGAGATGGCAAGGCGGCTTGCTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCTCAACTGGTGCAGAGCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTTGAGAGCTGGGCGAGCTTGCAGGCGGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACCAATTTGTGTCGCGCATTTGCCGATCTGCAAGGGCGATGAGGTTGGAGAGCGGGTG
CTTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCAGCGCCGACGATGGCTTCCCCTTCAAC
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGGTCTTCACT
TCCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTGCTTTCACAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCCCTTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCAGCCCGGTGCCCAACCCCGG
CCTGGAGCGTGATCACCACAGTGCCCGGGAAGGAAGATCAACTCATCTCCAGCTCCAGACCCGCTGCTGTG
AACTTCTCAAGGACCACTTCTGTATGGACGGGCGAGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCGTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCGCGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCCTCACACTCGGGCGTAGTCCAG
TGCCCATGGCCAACTGCAGCTTACCCGAGCTGTGGGACTGCTCTCTCGCCGGGACCCCTACTGTGCTTGG
AGCGGCTCAGAGTGAAGCAGCTGAGCTCTACAGCCTCAGCTGGCCACAGGCGGTGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTTCGGTTGTGTCCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCCAGCCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTTCCAACCTGGCGACCCGA
CTCTGGCTACGCAAGCGGGGCCCCGCTCAATGCTCTGGCCCTCCTGCCAGCTGCTACCCACTGGGGACCTGCTGCT
TGGGGCACCCAACAGCTGGGGGTTTCCAGTGTGCTGCTACAGGAGGCTTCCAGCAGTGTGATGCCAGCTAC
TGCCCAAGAGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
TCGCGTGTGAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCCCTACTGGAAGGAGTTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA
GTCTTCTGGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC
CCACTCAAGGCTAGGGGCCCTAGCAGCCCCGTGATCACCAGGGTACCAGTCCCTGTACAGACAGCCCCCG
GGGGCCCGAGTCTTCACTGAGTGCAGAGAAGGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGATCCCCAGTG
TGCCCCCGGCCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGGTGAGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGGTTACAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGTGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTAAAGTAGCGAAGCTCC
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCCTGGCCAAATATGGGGCTGCTAGGTGTGGTGAA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAAACAAATCCAATGTGAACTAGAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGTGG
TTGTCTGAGACAGAGTTGGAAACCTCACCAACTGGCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCGAGATTGAGACCAAGCTTGGGCTGCGTGCGCTTCTGCCTTGCAGCTCAGCCGAGGATGTAGTTG
TGCTCCCGCTGCTCCCACCACTCAGGACACAGAGGCTAGTTGGCATCGCGGCTCACCAGGCTGCTGGGCTC
GGACCAACCTCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCTTTCCCTCAGAATTACAGGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA
GAACCCGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCGAGTCCCAAGTTCAACCTCCATCCCTCACCTTCTTCACTTAAGGGATATCAACACTGCC
AGCACAGGGGCCCTGAATTTATGTGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCAATTTTTTAATAA
GCTGAAGAATTACTGTTTAAAAA

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FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAIEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSPDD
GFPFNVLDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSILYQPQLATRPWIQ
DIEGASAKDLCSASSVSPSFVPTGEKPCQVQFQPNVTNTLACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLILLVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQDDEGGSPVPII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLEVLFLLYRHRNSMKVFLKQGECAV
HPKTCPPVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPVRVLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 455

TAAGATGAGGGGCATCCCTCACGTTACACCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTATAGGACTGATCCCTTGACAGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCAATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCACTCTGGCCAGTTTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAAGTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCCTAGTTTCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTTCAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGACAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCTC
CAGGGTTTAAAGCCGGCCATGCCTTCCCAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCACACAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCTAACAGCAGCCTGGAGCTACCCCAATCCCTCACAGCCTGACCCTCCTCATTCATCA
GATCTCGTGCCG

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FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPORTGSRAWVVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

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FIGURE 457

CCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGGCCGTGGCCCGGCTCTGGGGCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCCGGCACAGCCCGGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCC
CTTGTGACCCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTCT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGGAACACACCGAGGACGGCTCAACATTTCATTTCAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCCTT
GAGGCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTTCAGCATCACAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTTCGACATGACTCGCACCCCGTGG
GCTGCCCCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCTCAC
GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
CTGCTGACCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGG
AACTGTGGGTACCTTTGAAGAGGGCCCTTCCCCTGCAATTCGTGCTCACCAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCGGACCTTCGCAGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGATTGATAACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; 'NX(S/T)': 6
MWGLLLALAAFAVAVGPAVGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRNLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFFANS DPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEGHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYE IAYHRGSELVG
WAEGRWNNQSIDLNNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR
AVIKWMMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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FIGURE 459

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAG**ATGA**AAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTCGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCCTTCCTAGCGAAAAG**TAA**ACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 460

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLILLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

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FIGURE 461

AGCAGGAGCAGGAGAGGGACAA**ATG**GGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAAGTTGCTGCAGAAAGTTGAGAAATCCTCAGATGGTCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTCAAACATAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGA**ACTCTGA**CTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCCCTGTCTTAAATCTCGTTTTCTCTTCTTCTTTTAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTTCATACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCCCTGCTCTTTTAAGGTTACCTAAGGGTTGAACTCTACCTTCTTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

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FIGURE 462

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKEPGVSFGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVQIHLLIMNKASPEYEENMHRYQKAALF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVEHVQNFCDGF
LSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

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FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTACGACCCACTGAAGACTACGACCATGAAATCACAGGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGT**CGCTAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

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FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSFPVGR
```

Signal peptide:
amino acids 1-22

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FIGURE 465

CGGACGCGTGGGTCCGGCGGCCTGAGGCTGCACCGGGCACGGGTGGCCGCAATCCAGCCTGGGCGGAGCCGGAG
TTGGCAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGT
TGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGC
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAGAACCACAGGCTGC
TGGCCCCAGGATACATAGAAACCCACTACGGCCCCAGATGGGCGAGCCAGTGGTGCTGGCCCCAACACACGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG
GCCTGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCGAGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
AAGTGTACATTGTGGCAGACCACACCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAAAACAGCGTCTCC
TGGAGTCCGCAACTACGTGGACAGCTTCTCAGGACTCTGGACATTCAGGTGGCGCTGACCGGCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCTCACGCAGGACGCAACGCCACGCTCTGGGCCCTTCTGCACTGGCGCCGG
GGCTGTGGGCGCAGCGGCCACGACTCCGCGCAGCTGCTCACGGGCGCGCCCTTCCAGGGCGCCACAGTGGGCC
TGGCGCCCGTCCAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCG
CGCGCCGAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCGACGGCTGCTGCGTGG
AGGCTGCGGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTCAGCGCCT
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCTCTCCAATGCCCGGACCCCGGAG
TCCCGGTGCCGCGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTTGCTCACAACCTGCTGCTGCGCCCGGGGGCCAGTGCGCCACGGGGACTGCT
GCGTGCGCTGCTGCTGAAGCCGCTGGAGCGCTGTGCCCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT
GCACGGGCACCTCCTCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGACCTGGCT
ACTGCTGGGATGGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCACCCAGCTC
CCGAGGCCTGTTTCCAGGTGGTGAACCTCTGCGGGAGATGCTCATGAAACTGCGGCCAGGACAGCGAGGGCCACT
TCTGCGCTGTGTCAGGGAGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
CGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGACTTGTGCGGGAGCCTTGGCACTCC
CCAGTGCCACAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTTGGACCTAGAATGGTGTGCC
AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCACAGCCACGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGTGGCCCTGTGTCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGTGCTG
CTCTGCTCCCAGGGGCGCGCTGGCCTGGTGTGTACCGACTCCCAGGAGCCCATCTGCAGCGATGCAGTGGG
GCTGCAGAAGGGACCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCAACCCCTGGGCGGCGTTTACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAAGTCTCATGAGCCAGCAGCC
ACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCAAGCAGATCAAGTCCAGATGCCAAGATCTGCTCT
GGTGAAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAAGTG
CAGGGGCGAGGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCGAGTGGAGCT
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT
CTCCAGCTCAATAAACCATCAGTCCAGAAAGCAAGGTACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG
GTAGTGTGGCCATCCAAAAGGGCTGTGCTGGGAGTCTGGTGTGCTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGCGATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACTCC
CCTGCAGCCTGGTGGCCTCTGCAACAAACATAATTTTGGGGACCTTCTTCTGTTTCTTCCCACCTGTCTT
CTCCCTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGAC
AGCCTCTCCCCATTCTGTGTGTGTCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAGTAGAAGTCAA
AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCATAATCCCAGCACTTTGGGAAGCCGGGGTAGGAGG
ATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAAGCTG
AGTTCAACACTGCAGTGAGCTATGGTGGCACCCTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCTAA
AATAAATTTTAAAGGACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA

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FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRRARGTPLL LLLLLLLLLLWVPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLPEVPVSKPDMGLVALEAEGQ
ELLLELEKNHRL LAPGYIETHYGPDPGVVLAPNHTDHCHYQGRVRGFPDSWVVLCTCSGMSGLITLSRNASYYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFQGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECDLCCFAHNCS
LRPGAQCAHGDCCVRLKLPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSFCARGSGYCWDGACPTLEQQ
CQQLWGPGSHPAPEACFQVNSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRRCRKNFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPAGLAWCCYRLPGAHLQRCSWGCRDRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSLW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metallopeptidases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

CGGCCAGGGCGCCGACAGCCCCGACCTCACCAGGAGAACA**ATG**CAGCTCGGCACTGGGCTCCTGC
TGGCCGCCGTCTCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAGTGCACGG
GCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTCACCACTG
CCACCCGGGTCTCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATAGGCT
GCCCCGATATCCCCAGCCTGGGCCCTGGGCCCCTACGTATCCATCGCTTGCTGCCAGACCAGCC
TCTGCAACCATGAC**TGA**CGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCCACAGCCCC
CACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACCTCTCCCG
GCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTTAGGGAAGTCTCTGCGTGGAGTCTTGCCTCA
ATCTGTGTGCCGTCCAAGCTTGGGGCCCATCGTGCCCTGCCGCCCTTCAGGTCCCGACCTCCCC
ACAATAAAATGTGATTTGGATCGTGTGGTACAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYYSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

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FIGURE 469

CATGGAGCCTCTTGACGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACTAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCCTTCAGCGTGTTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGC GTT
CTCAGCTCATTGCAACCTCTGCCTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAAC TACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGTTATGTTAATGGAATAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACTATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

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FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFFPCNQFGGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

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FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTGCGGAGGGTTTCGTCAATCAACCTCCTTCCCGCAAACCTAAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
ACCGGGTTGGCGCTGCCCAGTGGAAACCGACAGTTTGCGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT
GTTGTTCACTGTGCGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTGCTTCTTCTCCTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
GGTCTACCGAGACCGATCCGACGCGTTTGGCCCGGTGCTGCTTATGTCATCGGAGACCCCCGAGCACCGGCGAA
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGGCGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTACCGGACAGTTTCAGTTTCGCCGATGGGAAACCCGGAGACCAAATCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTCACACGCGTACAGCCA
CAGGTGGAAAAGAAAACCTTGACTTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAAGACTCTCCTGA
GCCAGAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT
CGATTTTCCATTTTATGGCCACTTCTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTGATCCCAGTGTATCCAGAAA
TTCAACTGTCAGATATTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
TAACCTGGGAAGCTTCACATTCAGGCAACCCCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTCTGTTGCCA
CAGGATCCAACAAATTCCTAATGTTTGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
AATTACCAACATTTTCGGCTGTGGAGATGACCCATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCTGTGT
ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGTCCTAACTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCCACGACCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT
GGTCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCCAAGCAGATGGCCTGCGATGAAGTTTGAAGAGGCTCTGGACATCCTGCCTATGCTGA
AGTTGAACCAGTTGGAGAGAAAGAAGGCTTTATTTGATCAGAGCAGTGTAAATTTCTAGGACAGAAACACACC
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCTATACCTTTAAGACAAACAAACAAACACACACAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
AAAATAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCTAGTGAATGTATCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
GGATCAGAAAAAAAATCATAATAAAGCTTTAGTTCATGAGG

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FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEEVEVD SHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSETDLLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS
ASRDLWVNIDQMEKDKVKI HGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSETFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTVGATTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTILHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCCGACCT
GCAGCCTCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTC
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCTCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCTC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTGAG
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCCCACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGGCTCCCATCCATG
TGCTGTGAGGAGGCCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTCTCTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTCCAGAAATAATTTTCATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTTTCTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTCCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTTGCCAGAAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTTGACCAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTGATTGATTAAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCGTTTCAGTCACAAAGCAGGGAATGGTTCAATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTTCCT

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FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHRFKEDWGFQKCKPCLDCAVVNRQKANC SATSDAICGDCLPG
FYRKTCLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILLCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCCEEACSPNPATLGC VHSAA SLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENF TAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

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FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTAAAGTAAGAATTGCAAAA

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FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTILVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSPVYIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGATTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT
TCTTTTTCTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAGGGT
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAAATGGATGATCCCTTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAACTACACGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCATGACAATGCCCCACA
GTTTGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCCCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCATTTTTTGATGCCTCAGAAAATATTGCAACGAC
CTTTCAAATCAATCCTTTTTCTGGGGAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATTCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGTTTTAGTGGAGTATTGGACACCAA
TGACAATCCCCCTGAAGTATCGTATCATTTTTCCAATCTGTGTGCTGAGAATTCCTGAGACGCCGCTGGC
TGTTTTTAAGATTAAATGACAGAGACTCTGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACATAACGGTCCTGGT
CTCCGACGTCAATGACAACGCCCCCGCTTCACCCAAACCTCCTACACCCTGTTTCTGTCGCGGAGAACACAGCCC
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCACGCCCAGGTCACCTACTCGCTGCT
GCCGCCCCAAGACCCCGCACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGCCACCTGTTGCCCT
CAGGTCGCTGGACTACGAGGCCCTGCAGGCTTTTCGAGTTCGCGTGGGCGCCACAGACCGCGGCTCCCCGCGCT
GAGCAGAGAGGCGCTGGTGCGCTGCTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTGTAACAGCTGCTCAAGGCCACGGAGCCCCGGGCTGTTCCG
TGTGTGGGCGCACAAATGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGGACGACGCAAGCACAGGCTCGT
GGTGTCTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGACGGCTT
CTCCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCCGGCCAGGCCAGGCCGAGGCCGAGGCGGACTTGCTCACCGTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCTGCTCTTCTCCTCTCGGTGCTCCTGTTCTGTTGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTCGGTGCCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCCTGTCCCAGAGCTACCAATGAGGTGTGCTGACGGGAGGCCCCGGGACCAAGTGAAGTT
CAAGTCTTGAACCACTTATTTCCGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT
CCGAAATAGCTTTGGATTAAATATTCAGTAAAGTCTGTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTTGCATTAATAACAACCTGGGTTTAAATTTAATGAGTATTTTTT
CTAAATGATAGTTAAGGTTTTAATCTTTTCAACTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA
ATCTGAGGTTTTGATTCATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGTCTTA
TTTAAGAAGGCATATCTACATTTCCAAACTCATTTCTAACATTCTATATATTCGTGTTTGAACCAAGCATGTTA
TTTCTACATCATGTATTTAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCCTTAGTTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTTATGTTAACTTTTGTGATGTATAAAACAGACTATGCCCTATAATTGAATAAAATATATAA
TCTGCCTGAAAATGAATAAAATAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 478

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVVLDVNDNAPOFAQALYETQAP
ENSPIGFLIVKVWAEVDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTEHNITVLV
SDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSTNAQVTYSLLPPQDPHLPLASLV
SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFSQPYLPLPEAAPAQAEADLLITVYL
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGFPFPHLVDVARGAETLSQSYQYEV
LTGGPGTSEFKELKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**ATG**GGACCTGTGCGGTTGG
GAATATTGCTTTTCTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGACAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCTACAAAATTTCTCTGTGAAGGTCATGTGCTCCAGCTGCTGAAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACCTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCTGCTCCTAGAGATG
AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCCAACCCCAACCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCACCATATAGTTTTATAGGTGCTCAACTTCTATATCGCTATT
AACTTTTTTCTTTTTTCTA

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FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSR TGRSREVLE
LGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQT MATLKGL
VQKGVKVDLGIPLLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEGHVL
PAAETACLQETWTGKEITDGE EKTEGEEEEEQEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:**Signal peptide:**

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

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FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTCGGGTAAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTGCGGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTTGGTCGGTCAAGACAGGTGTGCTGATGTAACCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACCTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCCATTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTGAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTGTGTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCTGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGGCGTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDIIEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWIEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

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FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTTWAERALRENERHAFTCRVAGGPGTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQGPVTVNTSDFLVLDQAQNPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGCGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTCTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAAACAGTGAAGTTTGTGTTGACTAAAAAAA

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FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLETSTILGTYVEAGAAKSNEEEIVNKSEFGRFPGRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

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FIGURE 487

CGGGGACGGAAGCGGCCCTGGGCCCAGGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACT**CTGA**GTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

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FIGURE 488

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSFAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGGATCACTGTGGTGCCCTTTTCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCAGGGCTACAACCTGACCTTGCAGACACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCGGGGTGAGCACGCCATGCAAGTTCCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACTC
ATCTCTGCTGAATAACTACGTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAGCCTGGAAGGCTACACCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTGACAGAGCAGCCCTCCACTCTCAGGTGCTCTGCCGCTG
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTGCTGCACTTCCATT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCTGAACATCGCCTT
CCTGCTGAGCCCCGATTTCGAATGTCTCCTGTGCCCGGGTGCAGCATGCACGGCTCTGGCCGCTGCCCTGCAC
CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCTCGGGCGTGTCTACAA
CAGTACATCCGCAGATATGTGTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT
CCTCTCTGTCAAGAGCTCGGTATACGGACCCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTCTATGGGCTACGGCGGCCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCTCACCGTGTCTGGGAACCACTGGGCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCAGCTGTTCTCTTACCATCTTAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGTTTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCTTTCAGCTC
CTCCCAAACAACACAGTAGTCCGGGCCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGAACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTT
CACTTCCAGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACTTTGTCTGTACCTGGGCCCAGCTCGCCAGGGATGTGGGCAGAGCACCA
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGCCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGAAGCAGCTTTGTTTACGCCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGAAGAGTGTGAGCGTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGTAGGGGC
AGGATCTCATTAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCACCCCTTCCCAAAGATTGGGAGGTTCCGCCGTTCCAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTTCTTGGGGCA
GAGGAAAACGCTTCTTTCTCCTCCAGCTGAATCAGCTGGATCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTGGAAGCTCAGGCCATAGTTTTCAGAGAATCACCC
TTACCCACAGACCTTATGAGACAGTGCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGGCGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
CAGCTGGAGGGGCCGTAAGTGCAGGACTGCGCCTACTGAGTGACCCATTTCTCCAGGAGGAAGGCAGACAG
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACCTTTCGCTCTTGGGGGCTGCACCCACAGACATAGC
TGGCACACAGAGCAGGGTGTCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCGGTTTTGATGACCT
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCTCAGTTTTCC
TATTTGTAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAGAATTCAAATAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

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FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQLNATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHMQFFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNI AFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSLSVKSSVYGPCTIPVFDWENGTFQNMSCWVRSPVHSLVVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTO
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

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FIGURE 491

CTTGGCTGCCCCGACAAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTCCGACACGGGCTGCCCTGAGAGACATTTC
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGAGTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCCCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACCTCAC
TCTCTATAACCCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTGAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGAAAAATACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTACAGTT
ACCGTCATGTACCACACGAATTCAGCCAAGGTGGTGGTCCCATAAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTAAAAATAAAAAA

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FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDSLTTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSFEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGAGAAGTGTAACTAGGGCTACTGTTGATTTTACTATCTTC
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAAACTCATTAAATGCTGCAAACTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTTAGTTACACCTGAAGTACCTGTTTCAAACAGGAATAGAAGT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTAAAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCAATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTAATGGATTCTCATT
CATACCCTTGTATAATTGGAATTTTGGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
AATGAAAACCAAATTTCCCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
TATCCTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTAAATGGTTATATAAAATTCCATTGTATAGTTATAT
CATTATTTAATTAATAAACACCCTAATGATGGATATTTAGATTCTTTTAAAGTTTTGTTTATTT
CTTTTAAAGTTTTGTTTGTGGTATAACAATAACCACATAGAATGTTTCTTGTTCATATATCTCT
TTGTTTTTGAGTATATCTGTAGGATAACTTTCTTGAGTGGAAATTGTCAGGTCAAAGGGTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
TTGTTTTAAATGTGCCTTTCCTAAATTTCTATTTTAAATAACTGTACTATTCCTGCTTCTACAG
TTGCCACTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAAATGGATTTATA

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FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTVCH
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDLHTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

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FIGURE 495

CCAGGTGCACAGCGCATCGCCCGAGGCTGTACCGCCCTGCCCCGCCACCCAGCTGTCCTG
GACCCAGGGGCAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACAGTACCACCTGCACCATGGG
GCTGTCCCGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCCACAGACATCAAGTTTGG
GATCGTGTTTGATGCGGGCTCCTCCCACACGTCCCTCTTCCTGTATCAGTGGCCGGCGAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCCAGAGGCCAGCATCGGAAAACACCCACGTTCCTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTCAGCAGTCAACCAGGT
CCTGGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCCTCCACCCA
GATCACGTTTCGTGCCCTGGGGGCCCATCTTGGACAAGAGCACCCAGGCCGATTTTTCGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGGCTGCCCTGCTCCGTCACCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTACCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCTCCTGCACGAGGGCTAC
GGGTTTCAGCGAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGTTGTTTCATGGTGTGTCCTGGCTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACTTAGTGGGAAGGCGGAGGT
GGGCCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGCTGCTGGCCACAGAGGCTGCATGACCTCCCCTCCCGGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCCTGG
GGGCTTCTGCTGGGCCAGCCCGCCTCCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAA

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FIGURE 496

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLLLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVWVAKVVMVLALVAVVGAALVQLFWLQD

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTCACCTGTCTCAGGAACCACCTGAGCCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCTGGTGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTTCATTG
CTGGTTTCGGAGTGC GCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCTTGGTGCAGAAGCATTAAAGCTGTCT
TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGCTGGCTGACAGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCCGTGGGTCTGAGTCCCAGATCCGCTATTCCATGGTCACTGGGCA
CCACTGTCAACAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
CCATCATCCTGCCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGCCCTCAACCTGGACATCACAGGGCAGCTGAGGTGCGATGACAACCTGCTGAACACCT
CTGCTCTGGGCGGGCTCATCCCGGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCTGCGGC
TGCAGCCCTTCGTGGAGGTCTTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAACCTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGTAGAAGCCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGAG**GCAAGACCACT
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTTA
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCCTCTGCCCCACCCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC

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FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLLAANFTFKVFRAPPELELTPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPPEMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

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FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**AAAGC
CCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCA¹AAACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACT**TGA**GACTCATT
CCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAA

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FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

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FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTGCGGTCCCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCTATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGTTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

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FIGURE 502

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLIFLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

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FIGURE 503

ACGGGCGCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
TCGGGCGCGTTCCCTTCGCGCGCCGCGGAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**
CGCAGCCTGCGGGCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT
GACCGCGGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTCAAGACAA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGCTCCTCGGCGGATTCT
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTTAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAAGTGGTGAATAGGATA
TTTGTTTGGCAGCAATAGAGCGGCAACACCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGAT**TAA**AGTAGAAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTATATTGCAGTTTTTGAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTAA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTAGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTTCGTTTATAAGAGGTAAAGGTCAAATTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

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FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO
LKCVGGTAGCDSYTPKVIQCNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSSEDQYVL
RGSCGLEYNLDYTELGLOKLKESGKQHGFAFSFYKSSADSCNMSGITIVVLLGIAFVV
YKLFSLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPHGGSG
SYSVCSNSDTKTRTASGYGGTTRR

Signal peptide:
amino acids 1-30

Transmembrane domain:
amino acids 171-190

N-glycosylation site.
amino acids 172-176

Glycosaminoglycan attachment sites.
amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.
amino acids 98-106

N-myristoylation sites.
amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

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FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTACCTTTTGAAGGACAAGATGCATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCTGAGAGACTGGCCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGTAGTTTCCTGGAAGACACATC
TGATTTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAA
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTTTATTGTGGTAAAAACACATCACGTAAATG
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCCGGAACTTTCTCATCTTGTAAATTCTGAAGTTCTATACCCACCGAACAACCTCCTCTT
TTCCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT
GGAAAAGTGTTTTCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTTATTTAAACAAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

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FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTTATTAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA
GACCCTCTTGGAACCTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTCTG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTGAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAAGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACCTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAA
GAGGGAGTGTTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTGTTTTTGACACACCAT
TTTGTAAATGAACTTAAGAATTGAATTGAAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAATAATTGGAAGGAGAGGGGAGGTCACCTCTTTGATGGTGGCCCTGAACCT
CATCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCTGGAGGTCCCTGGTTCGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

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FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYYTTEECMDKMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVG
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVVIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLKLKLVKEGVVKDLSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

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FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCCCTCCGCTCCAACATGG
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTTTCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTGTAAATTTACA
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGGTACACATCTGT
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

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FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLKAKSYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

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FIGURE 511

CAGCCGGGGCGATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCAGCCCCGTTCCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCAGGAGAGAGGAGCCTGTCACCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCGACACTGCTAGTGCCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCTCCTGCCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCACTGGACGCTTCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTTTAAATTAATAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAACTCGATCTCAGAGTTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAATGGCATATTTTAAATTTGGCCCAGACCAGAACCCAGTTTCTCTGGGATTAT
TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACTAACTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAAATATTAATAATACTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTAAAAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAATAATCTCTAGTGAACAAA
GACCTGTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAAGTAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGTCCTTTCACATACAAGAGGTGTTGCGTTTCATTTTGC GGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCCAGCTGTTGGACCTGC
TGCCTTAGAACCACAGATTGGTACCTCGTGCC

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FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCTGTTCGGGCCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTTCAGCCCATCCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTGCTCCTGCCCGTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCCTCCAGCTCAGCCACTGCAC
TGAGAACATGGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTACCGGGGATGCACGGTCTGCATTTTCGGCCCCCTGCGGGACAA
TGGAGGCCCTCTCTCCCTTTGTGCCCGGGCCCGGGCCTCTGCAGACAGACCTCCATGCCCA
GAGGTGAGAAATCAGATATAACCAGACATCCAGACCTCCTGGACGAGCTCCTGCACCCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCCTCAGTTCTTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTTACAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCCCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCCAG
TACACACAAGTTTTCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
CCAGCGCATCAACAGTGCAGTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCTC
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
TTCACAGGACTCAGCCCAGGTACCTCGCTGATTCTGCCCCCTTCCCAGCTGCAAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTGAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGGAATGCCATCTCGAGCCCCCTACAGCTC
TACGGGAGGCCTCCCAGAACAAAAGCGGAAGAGGGGGCCAGCCTCATCCCACTGCCAGCTG
ACCCTCAGTTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCCCGTATATGCAAGTTTTCCCTGCTGCCACGCAGG
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCAGTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

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FIGURE 514

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPGAGSHPFVGHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPLELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSIPAPFPAASMDA
GMRRTRHGTSAPAAAAAAPPRSTLNPTLGSLLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

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FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGCAGCGGCCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCAAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTCACAAGGAGGGGAT
CAAGCTTTAAGTAAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGGAGCT
AAGACTGTTTTTAAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCACCCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGGAGAGACCAAGAGAAACGAAGTCTTTC
CTTCAGGAGTTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAAAGAATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
TCCCACAATGCTGTCCACTACGGGAAGCATTTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATAACCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTAC
TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACTCTTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT
TTAATGTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTCATTTTCTAAAACCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAATGCATGAATATATTTTTTAGCAGTCTGTGGCATATTA
TCAAACCTGTTGAATTGTTTTCTTACACCCTGGAAATCTTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

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FIGURE 516

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKEHMPEDVREKKENLLLNSESTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKROGAKTVFNKFSNMNWPVDIHPLNKS LVKDNKWKKTEETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIYVEDKHKILYCEVPKAGCSNWKRI LMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGIIYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWKVKLCYPC
LINYDFVGKFFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTTPLL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

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FIGURE 517

GGAACTTCCAGGACACCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATGCCTCTGTCCAGCCACCTGCTGC
CCGCTTGGTCTCTGTCTCTGGCAGGGTCTCAGGCTGGGCTGGGTCCCCAACCACTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCCAGTGTGGTTACCACGGGGCCTCGCCCA
CCCTGGGCGCCCCCTTCGCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCTGGGCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCCTGC
GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCCTCTGGAGATGTGGCTGAACTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGCCGCATCCGGGGTGAATTCCGAGTGACCTTCTCTGCCACCCGAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCCACCCCCAGGCCAACTGTCCCCCGGGACACC
ACCACTGCCAGAACAAAGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGAAGACAACTGCGGGGACCTGTCTG
ATGAGAACCCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGGAACACCGTGTGGTGGTCTGAGCGCCCTCCTGGCCACGCCGTGACCACAGCCGGAACA
GTGCAAGGGCTCCTTCCTGCTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCCAAG
CCTCAGGCACCTCCAACCTGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCGGGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGGCAGACAGGCCCGG
GGGGCGTCTGGGTCTGGACGACCTCATCCTGTCTGACCCTGCAGACCAGTCTCGGAGGTGTCCACCCCTGCAGC
CGCTGCTCCTGGGGCCCCGGGGCCCCAGCCCCCAGCCCCCTGCCGCCAGCTCGCGGCTCCAGGATTCTGCAAGC
AGGGGCATCTTGCCCTGCGGGGACCTGTGTGTGCCCCCGGAACAACTGTGTGACTTCGAGGAGCAGTGGCGAGGGG
GCGAGGACGAGCAGGCCCTGTGGCACCACAGACTTTGAGTCCCCCGAGGCTGGGGGTCTGGGAGGACGCCAGCGTGG
GGCGCTGCACTGGCGCGCTGTCTCAGCCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCTCTGT
CTCTGCAGCGGGCCTGGGGGAGCTAGGCGCTGAGGCCCCGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA
GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAACGGCCACTTTGTGCTCCTGGACCCACAGCCCCCTGGCCTGGGGCCACAGTGCCCACTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGGCCCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTCCGCGTCAGGCACCCAGGGCAACCGCT
GGCAGGAGGCTGGGCCACCCCTTTCCACACAGCCTGGTCCCATGCCAGTACCAGCTGCTGTTGAGGGGCTCC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCCGTGCGGCCGGGCCCTGCTGGGGCCCCTAATTACT
GTCCTTTGAGGACTCAGACTGCGGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGGCGGCAGGCCAATGCCCTCGG
GCCCTGTGCTGGGGCCCCCAACAGACCATACCACTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGCCAGCCTGCTT
GTCGACCTTCTGTACACAGGGAGCCTCCGACAGCCAGGCACCCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGCCACGGCGGGCTTGCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCGCAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTTGAAGTCTGCGCTGTGTGGCTGGAGCCACCTGGCCGGGC
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGGAGCCACCCCTCTCGTTACCCCGAGCCCCCTGTGGACC
ACACCCCTGGGCACAGAGGCAGGCCACTTTGCTTCTTTGAACTGGCGTGTGGGCCCGGGGGCCGGGCCGCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCACATGGGTTTTCTGTGAGC
ACTTCTACAAGGGGGAGCTGAAGTACTGTGCAGAGTGTCCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGGCGGCACCACTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATGCTCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
AGCCTGCCCCCAGCCCGGGGAACACAGCCGCACCCGGGTCTGTGCCAGCTGTGGTGGCAGTGCCCTCCTATTGC
TCATGCTCCTGGTGTCTGTTGGACTTGGGGGACGGCGCTGGCTGCAGAAGAAGGGGAGCTGCCCCCTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTCAATGCGGATGGTGTACCCCTCCGGCATCTGTCA
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGCTGACATCCAGCACTTGGTCAGACCCCTAGCC
AGGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCTGGGCGTTCCC
TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACACCTGGCCCATGAGGGCCGCCCCAAAAA

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FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLPLALVLFFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDCSDEAQCQGYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETLTLWQSTGPWGPW
QELAVTTGRIRGDFRVTFSATRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPPSSRLQDSCKQGHLACGDL CVPPPEQLCDFEEQ
CAGGEDEQACGTTDFESFEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLPGSPGSCELHLAYLQSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPGQIGTL
RLAMRREGEETHLSRSRGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDLGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAWGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAERAWRVVFEAVAAGVAHSYVALDDLLQLDGPQPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPPQPPVDHTLGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCILRFWYHMGFFPEHFYKGEKLVLLHSAQGLAVWGAGGHRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCCQPAPSPGNTAAPGSVPAVVGSA
LLLLMLLLVLLGLGRRWLQKKGSCPFQSNTEATAPGFDNILEFNADGVTL PASVTS DP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077**Amidation site:**

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

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FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACATCAGCTCCTGGCATCTGTAAGG**ATG**CT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGGCAACAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCA**ACT**TACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGA**ACT**CACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTTCTATAGAT**TGAG**ACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

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FIGURE 520

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSMLRTMTRLCLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNNDNGPAIPVVYDFGDAKKTASYSPYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSAFDW
DGYGTHVKSSCSREITEAAVLLFYR

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

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FIGURE 521

GATCAGTGTGTGAGGGAACTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAGAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA
TAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCTGTGGAGACCTGATGGCTGAGTTGCTTGCACTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCCAGCTCCACTTTCTATG
TACCTGTGCTTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAGAGTAAAAATCAATGCTTTTCAGTTT
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTGGGAAGAGTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTGAATTTCTCAAC
CATACCAACCTAATTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTGAGGGGAAGATGGTATTGTGGTGTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTCCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAACTACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTGGTCACTCCAAACCA
AAGCTTTTACTCATGCTGGAATGAATGGGATCTATGAAGCTATTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCCTACTCTATAGATGTGA
TTGGGTTCTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTATTTCTCTGTCAAAAA
TTAATAAAACTAGAAAGATAGAAAAGAGGGAAATAGATCTTTCCAAATTCAAGAAAGACCTGATGGGGTAATCCTG
TTAATTCCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCTGTTGATTTTCTTAGGTGTCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTGA
TGATGTCACTTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC
ATGGATATAAAGAGGTAAAAAATTAATAATTCACAAAATTCAGTAAACCACACAAATCAGTAAGTGTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGTGTATTTCCATAGAC
CTCATCTAGATGTCATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAGGTGAACAGATATTTTGGGATTAGTAACTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATTCCTTATCTC
TATAATCAAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAAGTGTCTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAATAATTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGAATA
ATGTTTACACTAGTAAGCAATATGTTAATCTCTCATTTTTTTACTGTATATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAATATAAGTATTTTTCTGTGTATGTATACA
ATAAATATAAATAAATTTGTTTACTGTTTGAAGTTTCTTAAGTTTAA

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FIGURE 522

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLQLFCVCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER
SCGKLPAPLSYVPVPMTGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYSKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPVMGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAHD
LTFWQHYSIDVIGFLLTCVATAIFLFTKCFLFSCQKFNKTRKIEKRE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

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FIGURE 523

GGCTGCGGGGTGCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCTCCTGCCCCGGGTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACCTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGCGGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCTGTTTTCTGGTCTCACTCCTGGGCACTGGTGTCCTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCGGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTC
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTCTCCTCAGTCATCACCCTGGCTGTGGGTGAAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCTTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGGCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCTTGGGCACATCACTGTACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA
TCACAGACCCCAACCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATT
CAGTCAAAATTGTCTGTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAATGTCA

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FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSLOKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLE
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIIILLLLATDFLQGASWTSLOTTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGCLRKSCGIAGGDKTERRDSPRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTG NVSKI
NAAFGDNSPAYCPPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAATQEGEPTKEGADAVSGTQKGKTGGQQRGGEGQQSS
TLYFSATAE VATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKREL SHHA AVGVVWSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

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FIGURE 525A

AGTGCCCTCTGTCAATTAATCTCCACGGAGTCCTGAAGGTGCTTCCAGGTTTGTCCCATCACACAGATGAGGC
AATCGTTCTGTTAAGACTGTCCTTGGGTCAATATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGCACACGTGTGTGTTGCGTGTACATGTGCATGTGTGTG
TTGTGTGCCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATCCAACCCAGGAGGAGACTG
TGCTTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTAAAAATATTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAAAACATTCAAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGCACAGGGAACCTCTCCAGAAAGGCTGCAGGGCTTCCCTCCCAACCTCCAACGGCCCACTTGCTG
AGCCCGTGCTTATCTGTTCACTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
ACTCTGTGCCACGCTTGGTGCAAAGCCCCCTTGTGTGTCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAAATCTAGATGGAAATGGAGGTACGCAGTGGAAA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCTTCCATTCCACGCTACGCTGAAGCTCAATCTCTC
TTCTGCTTGAATCTCCCCCACTTCCCCACCCCAAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC
CCCATGAAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATCCAGTGCTTTCCTTGCTGAAAGAGAGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTTAAGCTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCCTT
GAAATACACCAGGCAGCTAAACATAATCTTTGCGTTTCCGTAGTGTGTTGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAACAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTGCTCCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCCTATCAGGGTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGCTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGGAAATGCAACATATTTAGATGGCACAACCTAATTAGATTT
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACCTACG
AGGGGGTTTCGTTTTACAGACTATGATCTTGCATGATTTCCCAAGATGCTCATTAGTATATGGTGAAGTAGA
ATTTGAATACAGAAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTTGGTTCAAACCAGCCTTCTTCTTTCAA
ACAACCTTCAGTGCAATTCATGTTTTGGAAAATAAACTTGATTTTGAGATTCAGACAATAAGTGCAATTTTTAATG
TTTTATTCTTTTATCTTGAAAACTGATATATTTTATGAAATGATATGTGCTCACTCAGTGTCACACTTCAAACAA
CACAGACAGTACAATGACAAATTGGAGATCAGCTCTAATCTCGGCCCAATTTAATGCATTGCTGAATATTCTT
CTGAACATAGTCCATCCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAACTCTTGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAGTTCTGCACCA
AATAACCCCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGCATTTCATCCAGCA
GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAAGAAACACACAGGTACTTTAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCATTATATGCTGGCACCTGCCTTTTTTTG
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTTACCATCGTGTTTAAATTTCTGCAGAGCA
CTTATTCAAGCATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCACTTCTGAAATGATCTCCTTAGAATAAATTCCCAATTTGATTGCTGGGTTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCCATTTTCTTAAATGCTTACTATGACTGGTTTCCAACCTACATTTTAATTTCTGTTCAATCTGATAGGCAAA
AAATGATATTTAATTTTTATTGATTGATAATGACCTTGAACGTGCCCATTAGCCTTTTGCATGATTCTTTTAT
GAAACATCTGTTCTATCCTTCGTCAATGTTCTCTTCATATGTTAACTTTTCTTATTGATTTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGTCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTCAAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGTCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATTTCTCCATATTTGCTCTTAGCATTTTTTTTCT
TTTTCAATGTAACCTTTGTTCTTTTCAAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTTT
CCAAATGGTGATTCACTGTTCCATTTCCATATTTCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA
TCTGCGTACTTGTGTCCCTTCTATAATCTCAGTTCATCTCTTTGAGCTATCTTTGATTCCCTTTTTCAAACCAC
ACTGCTTTACTGAAGTGTCTCATCTTATACATTTTAACTACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTCTCTGGATAAACTTTAGAATCACTCTTTTGTCCAAGGTA
AAATATATCCCACTGAGATCATACTGAATATACAGACTAATTCAGGAAAAATGTATGCTTTTATGCAATGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA

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FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTAGGTATTTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTAAATAGTTTTTCTATTATTTGGGTTTTCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTCCAATGTTTCATAACTGTTTTTATATTCTTGCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

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FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

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FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTGGACAATTGTCTTGATCATAGTTAGTTGGACAACT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACCTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAACTTAATCCTGATCCA
TGTAACCTTTGGCATTATCCTTATTCGACTATGGCAATTCTTGGAAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCATGCTTTGTCTTCATTCCCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

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FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYFFK
LNPDPCKPLAFILIPMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

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FIGURE 529

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCTACAACACTGAATGGAGGTCAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAAACCCAGTGCCATGGCAGTGGAGTCATTTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTCTCTCGTCAGGCCTCATCGACAAAGTCGACAACCTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTCGCGGTGGAGACTTTTTCTAC
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCGTGTCTCCTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGGCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTACCTGGGAGTGCTTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTGAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTCACTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGGAACACAGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAGTTTTGTAATAAATTTCTAAATTATCA

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FIGURE 530

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSQPGFLERLSETSGGMFVGLMAFLLSFYLIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKKLRRHVE
MYQWVETEESEYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVOIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLPAPHVTVIARQRGDQLVPFSTKSGDTLLLLLHHGDFSAAEEVFHRE
LRNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFACVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE
```

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

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FIGURE 531

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTCTCCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTCAGA
TAAGACTTCACTGAGTGACTGTTGAGCCCATGATTTACCCTGCAGTTTAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTCTGCCTTTTCACTATTACATCCCCGCCTGTAGCCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTGCTGAATGATAACCAATAA

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FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGTSGIRSHQLSAGHLGL

Important features of the protein:**Signal peptide:**

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

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FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGGCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCTGGCCGCCTCC
CTCTTCTGGGCACGTTCTTCAATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAAACC
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCCTCTGGGCTGTCCTCCCGCTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCATTGTGCAGAAAAGTCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTGCTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 534

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMNTAQLPECCVDVVGVNASCPGASLCGP GCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPG EAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPI PAPP

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGGAGCGCC**ATGG**
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGTTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTTGCTACTAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTTCTCCTACACATACAGGCGGCCCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTGAGTTG
TGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTTT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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FIGURE 536

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLELLVRLVNEVNFLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTNGYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY
PNAQIYVTTEKRMSYCDGVFKEKTKDSTE

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

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FIGURE 537

GTATTATTGACAATACATGCATCATATCTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCCTTGGTGGTGACTACACCTAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTGGACAGGAAGCTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTCAAGCCAACCTCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCTTCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAGAAAGAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTGGTGAGGATTGTCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAAGTTCCTTATGTCCCATGGATCTCTTCTGATCTTCCCTGCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

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FIGURE 538

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVTTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFRFT
WRLARGVISTDDEVFKPFQANSHFVKFKYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGC**ATG**AAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCT**TAG**TACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

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FIGURE 540

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

FIGURE 541

CTCCACGAGGCTGCCGGCTTAGGACCCCCAGCTCCGACATGTCGCCCTCTGGTCGCCTGTGTCTTCTCACCATCGTTGGCCTGATTCTCCCCACGAGGACAGCGTTGAAAGATACCACGTCCA GTTCTTCAGCAGACTCAACTATCATGGACATTCAGGTCGCGACAGAGCCCCAGATGCAGTCT ACACAGAACTCCAGCCCACCTCTCCAACCCCCAACCTGGCCTGCTGATGAAACACCACAACCCC AGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACA AGAGCACCAAAGCAGCTCATCCCACTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAA GCACAGACGTCCAGACAGACCCCCAGACCCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCT TCTTCTATGATGAACACACCCTCCGGAAACGGGGGCTGTTGGTCGCGAGCTGTGCTGTTTCATCA CAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGTTATGCCGGAATCGTT GCAGGTGAGTCCATCAGAAACAGGAGCTGACAACCTGCTGGGCACCCGAAGACCAAGCCCCCT GCCAGCTCACCGTGCCCAGCCTCCTGCATCCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACAC AGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCCTGCCCGCCC CTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAG TAAAGCACTGTGGTCTTTAAAAA

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FIGURE 542

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELOPTSPT
PTWPADETPQPQTQTQOLEGTDGPLVTDPEHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTS GKCRQLSRLCRNRCR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

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FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGGCCGGCCAGTCCC
GCTCCGCCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTGAGGCTCATTTCCAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGT**GTAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

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FIGURE 544

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCQAHSONVTFVL
RKVNDSGYKQEQSSAENAEFFFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

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FIGURE 545

GGCGGCCCCGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGACCCAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCAGATTGGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAATCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAATCGTTTAC
ATCCACCCCTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAATGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTAAACCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

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FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81; NX(S/T): 2
MMLIPMASVMAVTEPKWVSWSRFLWVTLLSMVLGSLIALLLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSTSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKVMSIPKGNSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRRTTQVLVGHHPHPQDVEKQMQEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDDYHVLEAANEQDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

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FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTGAGTCCAGGGTGTG
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGACTGGAGGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGGCCAGGGATCTCTGTCC
ATCTTGTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACCTTCCTGATGGGTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTTGGCAGGGGGACAGGAGACTGTAACAGGCCAGGTCTTGTGACGCCCTGAATGC
ACGCCCGCCTTCGGTCTGTTCCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTTCATGCCAAAGTCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCACCATGCGG
GCCTCAGGTGGCAGAGAGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTAGGCAGGCCAGCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCACCCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCACCCAGCACCCGTCCCAAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAACT
ATGCATTTCATTAGCAATAAATGAGCCTTTGCTGCA

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FIGURE 548

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAPTDSTY
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPNAGILAATIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMMATTEKPELGPAGDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCQLVPTS

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCCTTCAACACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCACTGGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGCTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTCACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGGTGGTGAATTACACCCCTGTGTTACACATGAAAACCTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATCTCTCTCCTCTTC
CTCCAGTCACTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTCGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACTTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTCTGCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCACTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTTCATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTCAGCA
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGAGTTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGAGTTCATACACGAAG
GGCGTGTGGCCATCGTGTGAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT
CTGTCTAGTTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCTCGCAGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCGTTACAGTGGAGCGTTCGCTGTCCATAAAACGTTTTCTAACTG
GGAA

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FIGURE 550

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVL MVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSP TARAGPGQAWSLRC
VLVGILHSDRR CALPTFP HSSFACGAHPFAESSFPCGLWPAEVK

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

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FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGACGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
GACCCTGGCCCTGGGTACCTTGCCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCAGGCCTGGTGAAGTGCACCTG
GCTGTTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTACCAGCCCTTCTCTGTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCGCCGGTTGGCCTCAGCCCCATGCACTTCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGCTGT
GCCCCACCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCT
ATTCATGGACGGCAACTGTTATTACAAGAACCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCCGCAACCTGCCCTCCAGCCT
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCGCGCCTGCGACCAAGCTCCCAACCCCTGCATGGAGTGCCTCGTCACTT
CCCCAGTACATCCGATACCTTCAAGCCACCTGAGCCGCTCTGAAGGCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGTGGAGTGGTGAAGTGAAGTGAAGTGAAGT
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
GAGGGTGTCTTTGCCACCTGTCTTGGCCCCCTTCTTGGGAGCCTGGTGGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTCCGCTCACTCGATGAGACCAGCTCCGGCCACTGGCCCGCCTGCCATGTCCAGACTCTGCG
TCTGCAGATGAAGTTCATCAACCAGGCCAGCTCGGCATCTTCAAGGCTTCCCTGGCCTGCGTACGTGGACCT
TCCGGACAACCGCATCAGCGGAGCTTCCGAGCTGACAGCCACCATGGGGGAGGAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA
CCTGCAGTGCCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCACTCAATGGCTCCAGTTCCTGCGCCTGACCGG
TCTGCAGGTGTAGACCTGTCCACAATAAGCTGGACCTTACCACGAGCACTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTGGCATGCAGGGCGTGGGCCACAACCTCAGCTTCTGTGG
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCCACAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCCTGCACACCCTCCTGCCCAAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCTGCCCCAACTGGAAGTCTCGACCTGGCAGGAAACAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGCCTGCAAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
CTTCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCACGCCGGGTGAAGTGTGGCAGTCCGGGGCAGCTCCA
GGGCCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCCTGGATGAGGOCCTCTCCTGGGACTGTTTCGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCATGCTGCATCAGCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCTGGCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGA
GTGCCGTGGGGCCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCCTCTTTGAGAA
CCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGGTCACTGGTCTCTT
GCGCGCCAGCTTCTGCTGGGCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGGTGTATCTGAG
CCCTGACGGCCGCCGCTCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCCGCAGAGTGCCTCCTCTGGCCCCA
CCAGCCAGTGGTCAAGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACTTCTATAA
CCGGAACCTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGAATCCTGCACGGTGCCACCTC

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FIGURE 552

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLVQAIMLAMTLALGTLPAFLPCELPQPHGLVNCNWLFLKSVPHFMSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPRLHLNLKWNCPVGLSPMHFPCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNLTVPRLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRRCDHAPNPMCECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWL
ASWFRGLGNLRVLDLSENFYKCIKTKALQGLTQLRKLNLSFNYQKRVSAHLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFTINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCSLTNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFQMGVGHNFSEVLAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLHTLLPQTLRNLPKSLQVLR
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDSWFGPLASALQILDVSNPLHACACGAFFMDFLLEVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMHLHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNEIRGQLEECRG
RWALRLCLEERDWLPKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016**Amidation site:**

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

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FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCGGGGTTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCGGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCATTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCTT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAAGTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTGGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGTGCTATCTGGAGTAATAGCTTTCATGGTGAAGTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTACCTATAACATGTTCCGACACTTCAAGTTCTGC
ATTACTTTATTTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAACGTCCTTAAATTGGGTTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVFTNLSLQNTTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFELGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFEGGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDP L SINQALGILCTLEF GILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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FIGURE 555

GT TAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTCTTCTGGAACCAGTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGAAGTCTAAGGCTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCAGATGCACC
TACTGCCCTCACCACTTGAACCCCCGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGTCAGCGGAGTTCACCCGTGTGGGTTCCTG
AGTCTCGAAGAGGGCGCCAGCTTGCAGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTGCGCAAGACGAGTCCGACGCCCC
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGCACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGCCCCACGCTCTCTGGACTGGCCG
CCTACCCCTTGCCCTTGGCGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTCGCGCCGTGGGCAACTGTTGGTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTTCGCCACCCGCGCCGCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCTCTGCACCTTCAG
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGGACAGTCCCTTCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCGGGCACCAAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCACCCCTGTCTTGAGCCCGTCTACCAAATAAAGTTGTAG
TGATTCCA

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FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLLELGHVLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLOAHRGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

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FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTT
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTTGACCCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGGAGGTTAGGTTTCGACCATTTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

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FIGURE 558

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVSVLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

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FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCGCCCCACGCCCCGATGCTCACCCTGGATGCCAACCCCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTACCTGCGCAGCCTGGTCCTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCCTGCGG
AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTGAGCTACAACGTCTGGAGTGG
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCTGGACATGAGCCAGAACCAGTTCCAGTACCTGCCAGAC
GGCTTCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTCGGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTC AAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTTTCAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCATTGCCAGACTGCCCCATTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
GGTCCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGGAATTGCTTGACCACCTTCCCAAGGTTTGGGGG
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTCTCATCGTCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCCAACCCCAACCCCG
CCCCCACCACCGCCCAAGTTCTTTTCCATCATTATAATTTCATCCTTATTATCTTGGTAAAT
ATTTATTAAGTGACTTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAAA
AAAAAAAAAAAAA

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FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTVGWRNRS GTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLH SCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEGL
ERLRELDLQRNYIFEIEGGAFDGLAELRHLNLA FNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLL PQYSKLR TLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITT VSLWEEFSSSDLADLRFLDMSQNQFQYLPDGF LRKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVP PG
LFANARNITTLDMSHNQISLCPLPAASDRVGPSPSCVD FRNMA SLRSLSLEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFFPRFGGSLALETLDLRNLSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLI LPSC
LTL LVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25; 74-78; 155-159; 232-236; 292-296; 309-313;
312-316; 408-414; 427-431; 500-504; 622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30; 39-45; 45-51; 141-147; 199-205; 245-251;
308-314; 396-402; 416-422; 420-426; 471-477;
484-490; 497-503; 522-528; 545-551; 555-561; 610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70; 492-514

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FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAGT
TTGGGCTGGAAGTGTTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAAGTTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTATTACAGCAAAGGATTTTCGTTGGCATCAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTTTGAGCC
AAACAAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLGALWWVPGQSDLHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSPVEESKKAEEVSQHREKSPVEESRGRELDVPV
EPEAFRADESDEGEGAFSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGESERTGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRRWHQNLSLFYK
DCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

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FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTGAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACTTCCTG
TGTTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACCTAGAAATAAACTGTTTTTCATGTTAT
GAAAA

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FIGURE 564

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLAFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEDSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

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FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCTGGGACCTGGGTTCCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

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FIGURE 566

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

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FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCACTGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

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FIGURE 569

GGTGCCAAGGGTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTCGCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTGAAATCTTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGCTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCCATTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCAGCAAAGAAAGAGACCGAAAGCAAAGTCATAAAC
ATGCCACGAGCTCAGCTGTCCTGCTCCGTGTCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC
TGTCTACTTCCCTGATCCTCTCTTCTGTGTCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCTCTGGCTCCCAAACCTGCCACTGTGAGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGGACTACACGTGGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTCCTCAAAATAAAGAGAATCTTTCTCCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFVSVDKLYDLLFTNSPFQRFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDFRHLSEELAKTESTYLAEMHRQ
SPKEKASKTTTVRRRKRPFAHLRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTTLTAWQGLRLQERLPQ
SQTEWAQQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

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FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAAATTCCTTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGCAGAAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAAGTGCATCGAGAGGGATGAGGTTCCGGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
GGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAGGAGCAGAAAGGGCTTCCTCCATGGCTGGCACCAGCCCTACATGGCTCCAGAAGTATTCAGGTTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCGGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCCTCCAGTGGTGCAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGCTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAAGGACAGCTG
CCCCGTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTCACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT
CCAGGACGGGTGCACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCACACTTGTG
CTGCTCAACAGGACTGCACCTCGTCTCTGCCCTGCCACCCAGAGCCCCCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAGCCCTGGGTTCTGGTCCCATCTCCAT
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCAATTAGGTAGGAAACATGAAAACCTTTGA
TATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCAAAGCAATCAA
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCTTCTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTCTCTGGCAGGCCACAGTCCCTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTACAGAGTCTC
CACCACCACCATATCCCCAGTGTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAAATCAGCACCCCATCCAACCTGGCCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTCAGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAAGTGGAGA
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTGAGAATCCAGCCCTGCTGGCTACTAAC
TAACTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTC
TGTGCAAAACAAACCTGTTTAGGATTTCTTCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
TGAAGTTCGACTGTGTTTTATTTTTTTCATCCAACCTCCATTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTCTTAGATTTCTTAAAGACATTTAATGTATGGTTAGGTTTTATATTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTCCTCCTTTCAACCGAGACTATTTCTGGATTGTGTCTCCTCGTCAGTTGACTTGT
TTTGACACACTTTTTCTTTACTTCATGTCCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTATTGGGCTGAGTTCACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGTTCTGTTCAAGTTGGCATTCTTGTGTTG
GAATAAACTATTTCTTGG

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FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD
VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDKSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQSLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

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FIGURE 573

CTCCAGTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAATAAATAAACGTC
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGCGAGAGG
AGACCTCAGCATCATCTAGAGCCAGCGCTGGCCCTGCCCTCCGCCCTGCGCCGCCGCCGCGCTCGCCGTTTTCTGTT
CCTGCTACTGTCCACCTAAACAACCTCCCGTTACACGGACAAGTGAACATCTGTGGCTGTCTCTCCTTTTCTTC
CTCCTCTTCCAACCTCCTTCTCCTCCTCCCACTTCCCAGCCGAGCAGAAAGCCCCAACCCAACTGACGCTGGCA
CAACTGCAAACGGTGTATCCGCACAACCTTTATCTCGCTCCTCGGGCTCCCCAAGGCATTGGACCCATCGCCGC
GTCTTTTATTTTTGCAAAGTTGCATCGCTGTACATATTTTTGTCCCGCCACCTCCCTCTGTCTCTGGAGTGCCC
TACAGCCCCGCAAACCTCCTCCTGGAGCTGCGCCCTAGTGCCCCCTGTGGGCAGTGGCGTTCCCCCCCATCCTCCC
GCGCCAGCCCCCTGCTGCTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCGAAGCGCTGAAAAGGAGAGACAGGAGGATGATGTCCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGGTGGCTTCTACCCCTCGGCTGTCTGCTGCCTGCGGAGTGACAGCCCGGGCTAGGGCGCCTG
GAGAATAAGATATTTCTGTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCACCTTTC
TCTCCACATTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGAAAGAGACCTAGTACTTCTCTGCTC
TGCAAAGACTATTGCAAAGAAATCTTTTACACTTCCCGAGGCCATATTCCAGGTTTCTCTCAAACAACCTGCGGAT
GAGTTTGTCTTTTACTATGCAAGAAAAGATGGTGGGTTGTGCTTTCAGATTTCGAAGAAAACAAAGTCAGAGGA
CCAGCATCTAACTACTTGGACCAGATGGAAGAATATGACAAAGTGAAGAGATCAGCAGAAAGCACAAACACAAC
TGCTTCTGTATTTCAGGAGGTTGTGAGTGGGCTCGGCGAGCCCGTTGGTGCCCTGCATAGTGGGGATGGCTCGCAA
CGTCTCTTCACTTCTGGAAAAAGAAGGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTTCAAGGAGCCTTAT
TTGGACATTCACAACTTGTTCAAAGTGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCAT
CCCAATTACAAGAAAATGGAAGTTGTATGTGTCTATACCACCAACCAAGAACGGTGGGCTATCGGGCCTCAT
GACCACATTCTTAGGGTTGTGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTGAGAACAGCCAGA
GTCTTTCTTGAAGTTGCAGAACTCCACAGAAAAGCATCTGGGAGGACAACCTGCTCTTTGGCCCTGACGGCTTTTG
TACATCATTCTTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTTAAGTGATTTCACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCCATACCAAGGAGCAACCCACACTTC
AACAGCACCAACCAGCCCCCGAAGTGTTTGCTCATGGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCCTGATATAAACATCAATTTAAGGATACTGTGTTGAGACTCCAATGGAAGAAACAGATCATCAGCCAGAATT
CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTGAATTCAGCCATTGAGTAATGGTCCT
TTGGTTGGTGGATTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTTAACCTCTCCAGCAAAGTCTGTGACAAAGCAGTGGCAAGAAAACCACTCTGTCTCGGCACTAGT
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTTGGAGAAGATGAACTAGGTGAAGTTTACATTTTA
TCAAGCAGTAAAAGTATGACCCAGACTCACAATGGAAAACCTCTACAAAATGTAGATCCCAAGACCTTTAATG
CCTGAGGAATGCAGAGCCACGCTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTGTGCGAAACGGC
TACTGCACCCCCACGGGAAAGTGCTGCTGCAGTCCAGGCTGGGAGGGGACTTCTGCAGAACTGCAAAATGTGAG
CCAGCATGTGCTCATGGAGGTGTCTGTGTAGACCGAACAAGTGCTCTGTAAAAAAGGATATCTTGGTCCTCAA
TGTGAACAAGTGGACAGAAACATCCGAGAGTGACAGGGCAGGTATTCTTGATCAGATCATTGACATGACATCT
TACTTGCTGGATCTAACAAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTCTATTTCAATGGGCATTTAT
TTTTTATCCTGTGCTATTAAGAAAAAGACTGTTATCCTGCTACACACTCCTGTGATTTCACTTCTTTTATTAA
TTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTGAGCATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTTGCATAACAGATGATTTTTTAAATATATACTTCTTATGCAAAGTAAT
TTACACAGAAATTCATTTGTAATTTGATAATGGATTTTTTATGTTACTAGAAGAGATTATTTGACTTCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCACTTTAATAGAGTTTGAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAAGGCAATATTTTTATATTAAGTACTATAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATTTGTAATCTTCATTTTTGTGAGTGATCCAGTTACAGAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTCATCTTAATCTCAAGATTGTTTTCAAGTGTTTATAATTAAATCAT
AATAGCATATTTTAAATCAAAA

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FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVSRSCSRQRRPQHHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFLLFQLLLLLPLPSRSRKPPQTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQ
LELLSGGEMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNNTCEGKLLLEEIKCALCSPH
SQSLFHSPEPEREVLERDLVLP LLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGL
CFPDFPRKQVRGPASNYLDQMEEDYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNGK
LYVSYTTNQRWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVDVDMCNVPYSIPRSNPHFNST
NQPPVEFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSESE
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLGPQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

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FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGACCTGCAGTTCTGCCCACACA
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCAGCTTTCCAGACAGTCACCTTTCCAGTGGTCATACCTGGTCTGGAAGATT
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCTCCAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGCAAGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCGCAAGCAACAAC
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTGAGACACAGGGGAAACC
ACTGCCTCTTTCAGTCTTCTCCCAGATTCCAACAGTCAGTGTTACAGCATTTACCTTGTTT
ACCTCCCTGAGAAGACGTTGCAGCTCACTACCCAGTGGGCAGTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCAGATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
CCGCTCTTCTTTAGTTCCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCACACAGG
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTCAGGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTTCACTTTCTTGATACCGTCTGGGAGGATTG
CTGGCTGGTTTCTTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTCAAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
TTCAGTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGCAAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATAA
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTG
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAACAA
CCCATTCTGCTCTCCTCTTCTCTTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
CTAGAAAAGCTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTGTCTCT
GAGATAAGGAGGAACCTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTGAGCCTTGGGGGACCAGTTACCCCTACATCCCAGGCTTCTGTTGTCCCTTGCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

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FIGURE 577

ATCGGTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAACTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTCTGATGATAACCAGAAAT
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTGAAGAGGTACGCAGGAAGTATATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTCCATCTTTGATTCACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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FIGURE 578

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

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FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACAT**ATG**GATACTTTACAGTTCAGGATTCCTACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTC AATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTT**TGA**AACAGCCATTTCTTCTTTTGGCAAACTGAAGAGGGTTCAC
ACAACTTATTTTAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAAACTACTCATTTCTTGGCATTCTTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTGTTGTGCAAAAAAAAAA

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FIGURE 580

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

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FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCCTTGTGTGTAGGGCCGCGTCCCACCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCAG
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCAAGAGGAGCTGCTGTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTTCCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCAGAAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATGTCTGTCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTGAGGAGCTGGAGTTGTCTTGCTGATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACCTGCATCGGGGCCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCCTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACCTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGATGACTGCCTTTG

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FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIIPECLQRAVHGILLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTITCG
TNPGLITKANELLFLHVEFDEVMFPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLTFFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

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FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGAGGAGCTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTGCACGGCAAATCTCGTGAACCTTGGGGGACGAAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCTCTCTTCTGCTTCAGAGGGAGAGCAGGCCGCTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTTCACTGGGACTAAGAGTGGG
CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAGGCTACACAAGCAGGCCCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT
CTGGTTGCTGGAGTTCTGCGAACCTGACATGTGCGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTTGGATGGAGCCACCTTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
GAGAGCACCTTAACCCCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCGGAGCCAGGCC
CTGCCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCAATTTCTGTGCCAGGCCACAGCCCAGCCTCCTGTACAGGGCTACAGG
TGGGCAAAAGGGGGCTCTCCGGTGTCTGGGGCCCCGGGGCCAAGGTTAGAGGTGCTGGCAGACGCCCTCGTTCTTG
ACTGAGCCCGTGTCTGCGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCGGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTCTCAGCTGCGCCTGG
CGCGGAACCCGCTTCCACGGGTAACTTGGACCCGCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCGAGGCGACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCTGCGG
GGCGGCGCCCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCTGCCTTC
CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGGTTTTTCGCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTTGGAGGCGGGGTGCGAGGGCCGGTTCTGGTGGAGACATTCCTTCCCCAGAGAGCCGCGGGGGA
CTGGGTCCGGGCTGATCTCTGTGTACACATTTTCGGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCGGTAGAGACTTGTGCCCCACTGTGCGG
ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCCATTGTGCACACTGACCACAGTGAT
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCAACCAACGGTTACTACAAGGTCCGAGGAGTCAGT
GTGAGCCTGAGCCTTGGCGAAGCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCCAGGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
CCCGGGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCGTCTCCAGACTCACGTGTGACAT
CTTTCCAATGGAAGAGTCCCTGGGATCTCCAACCTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCCTCCAAAAGTGAACACAAGGGGAGGGAAAGATCATTACATTTGTGAGGAGCATTTGTATA
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCCACCCCTGGCTCTCCCTGAGGGGAACCTTGTCTCGGCCAAT
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTTCTTAAA
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACCTGTTGGGGCAAAATATTGGGATAA
AAATATTTATGTTTAAATAATAAAAAAAGTCAAAGAGAAAAAAA

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FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHLHIREVELEDEASYEQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLTTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSASPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCEVSNAVGS
NRSTALDVLFGPILQAKPEPVSVDVGEDASFSCAWRCGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAAEARLTVNAPPVVTALHSAPAFLRGPARLQCL
VFASPAPDAVWVSWDEGFLEAGSQGRFLVETFPAPESRGGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTLMLVITGVALCCWRHASKAS
ASFSEQKNLMRIPGSSDGSSSRGPEEEETGSREDRGPIVHTDHSDDLVEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTPHPRAFTSYIKPTSFGPPDLAPGTPPPFYAAFPTPSHPRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

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FIGURE 585

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGGCTGG
CTGCAGATAACCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCCGAGAGCCGCCAAGGAAGAGAAA
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAAACCCCTTCCA
GCTCGATCTGCTCTTCGTCTGCTTCTTCCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
ATGCTGTCTGGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGTGTCGGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACCTGTGAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCTGGTGCCGCCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCCCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTGTCGTGCCACCAACAAAGCCATCCCCGG
AGGAAAGGAGACGTCGGTCACCATTTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACTTTCCACTGCTCTGCAAAGGCCAACCCAGC
TGTACCCAGTACAGGTGGGCCAAGCGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCTG
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCTGGAAGGAGAACGTTCTGGAGTCCGGGCACATCGGGGGCGC
TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAAGTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTGCGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCGTCCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCGTTCCAGAGAAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCCTAACAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTGA
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAAGTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
AAGAGCTGTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAAACCTTAA

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FIGURE 586

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCCLVLGYMAKDKFRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLKKEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAI PGGKET
SVTIDIQHPPLVNL SVEPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVLSNEKTLTLKSVRQEDAGKYVCRAVVP RVGAGEREVTLT VNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLES GTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKGAGLEAESVPM AVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATCGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAAGCATCAGAAAGCACAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTGAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCACT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCAATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAATCCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTCATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

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FIGURE 588

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLMSWLVCGSKL

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

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FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCCGCTTTCCCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAAACCCAGGGTGCTGGCGAGCCGCTAGCGCCATGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTTCGCTGCGCCTGCCGCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCAGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTACTCTCTGCTCCGCCGGCCGTTT
CGCCAAGTCCTGGCCGGCATGGTGACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGACCAAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCCTGCCTGCAGCAGACACACTTGA
GGGCTTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYS AELRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFFPLRYAGRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRMDTVMTKALALLADLHPSVRQCLIQQKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRP
FRQVLAGMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

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FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTTGTGAT
GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCACTAGAAAGCCAACCTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAAGAAATGACTCTA
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGTAGGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTGAGCTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
ATACTAACAACCTGGGGGGACACTATCTTCTCTATTGTCACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTGAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAACAGAGCCCATAAACTATGACTCTGAGG
TTTCATTGGAAAGAAAGTGTACTGTGCATTATCCATTACAGTAAAGGATTTTATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAGCTAGAG
CGTCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTGTAGTGTACACCAGCTGAATACGGAGCAATGGTGTATTAT
AAGCGTTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

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FIGURE 592

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYKLGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDET
FVCFDGGRRDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSSENTEDLQEQFTTQKHHSHANSQANHAQQEQASFESFEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDETTRLVTSLED
DFDEELDTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP
DSKQKGPKQSATDYSDFDNVDDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

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FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG
TCATGCTGCTCTGGGCTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACTCAGATTTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACGTGTGCCAAGAGCTAATCATTTCATACTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGACGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG
GCGAATTCTGCA

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FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80, NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCLMLLLIGLVTL
GMMFLQISNDINSDSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNPCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

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FIGURE 595

CGGACGCGTG GGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCACGGAATTAAATTCAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCCCTTCACT
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCTTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCCGA
AACAGTAACCTTTGAAGAATAAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWI SRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLA FQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPPLGRCICSTGYEEIEGSCHGASKGRCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

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FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGG
CAGCACAAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCTGTGCCCTGGTTCTT
GCTGTCCTTGGCACTGGGCCGAAGCCCAGTGGTCCTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCAATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCCGCTGCGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGCTC
CTATACTCAGCCCAGGTACGAGAAGGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGACGAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCTTCCCTGCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTTCAAGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAAGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGGCGGCCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTCCGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTCTGAACTGAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTTCTCTCCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGGGCGCACGGCCCGCACGACGCTTCCG
CGCCTCGCTCAGCTGCGTGCTGCCCCGACTTCTTGACAGGGCCGGGCGCCCCGGCAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCGT
CTTCACACTGCCCTCCCACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAAGCAGCCCTGGATAG
CTACTTCCATCCCCCGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAAGGGCGGGACCTGG
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGP
VLAPTHLQTELVLRQCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLSTFQAYPTARCVLLEVVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVNLVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPQIITLNLHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQLOECLWADSLGPLKDDVLLLETRGPQDNRSLEALEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRLKQDVRSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWFAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

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FIGURE 599

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTTCAACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATC**TGA**GGAGAGT
CCTTTAGAGTGACAGGTAAAGCTGATACAAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCTCCAGCAGAT
CATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTTTTGGCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLH
YDCGNKTVTPVSPGLGKKLVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTCTACCATGCTGAAGATAAACAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCGCCCTGACA
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCCTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAACTTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACCAGCAAATACACAAGGAATTCTTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTTCCCAACAGGGATGTCACCTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCTTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

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FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTS PRSRDCVAILNGMI FSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGACGCTCTGGTCTGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 604

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAGR
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPPFINLPALWRSVANIMP

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 605

GCACGCGCGGGCGGGCGGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATGG
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTAGAAGA
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTGTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW**Signal peptide:**

amino acids 1-20

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FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATG**TGGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACCTCTCCG
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCCCTGGCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCTCGGGATCGAGTGACT
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
GGCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCCGGCCCCGGTGCTTGTCTCCCCCTCCACCTCTTCTCCTCCTAGCT
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTGAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACGTGCTAGGGAAGTGGTTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCACCTGCCCACAAGCAAACACACCACACATGTTTCGGC
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGA CTGT CAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGTCCTTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCCATAATGGCCAGAGAGGAGAGTTTCGAGCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TGGAATGCTTTCCTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTCAACGTGATGTCATTCTTTCCACCGTTTCTTCTGTTGATATTCATGAATC
CGTCAATCTCTCTGGGAAA

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FIGURE 608

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFSLEPLTKDMAT

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

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FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142